

Serial Number: 10/038,010

CRF Processing Date: 8/6/02
 Edited by: DE
 Verified by: DE (STIC staff)

0590
0730

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____



OIEP

RAW SEQUENCE LISTING

DATE: 08/06/2002

PATENT APPLICATION: US/10/038,010

TIME: 13:16:30

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF4\08062002\J038010.raw

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3 <110> APPLICANT: HYBRIGENICS
4   Pierre, Legrain
6 <120> TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
8 <130> FILE REFERENCE: B4767A
10 <140> CURRENT APPLICATION NUMBER: US 10/038,010
C--> 11 <141> CURRENT FILING DATE: 2002-07-23
13 <150> PRIOR APPLICATION NUMBER: US 60/259,377
14 <151> PRIOR FILING DATE: 2001-01-02
16 <160> NUMBER OF SEQ ID NOS: 67
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 492
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: gene
27 <222> LOCATION: (1)..(492)
28 <223> OTHER INFORMATION: Human Skp1 : Part of SCF (Skp1/Cullin/F-box) complexes which
act
29   as E3 Ubiquitin ligases.
32 <400> SEQUENCE: 1
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35 gccaaacaat ctgtaactat taagaccatg ttggaagatt tgggaatgga tgatgaagga      120
37 gatgatgacc cagttcctct accaaatgtg aatgcagcaa tattaaaaaa ggtcattcag      180
39 tgggtcaccc accacaagga tgaccctcct cctcctgaag atgatgagaa caaagaaaag      240
41 cggacagatg atatccctgt ttgggaccaa gaattcctga aagttgacca aggaacactt      300
43 tttgaactca ttctggctgc aaactactta gacatcaaag gtttgcttga tgttacatgc      360
45 aagactgttg ccaatatgat caaggggaaa actcctgagg agattcgcaa gaccttcaat      420
47 atcaaaaatg actttactga agaggaggaa gccaggtac gcaaagagaa ccagtgggtg      480
49 gaagagaagt ga                                         492
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53 <211> LENGTH: 163
54 <212> TYPE: PRT
55 <213> ORGANISM: Homo sapiens
57 <220> FEATURE:
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59 <222> LOCATION: (1)..(163)
60 <223> OTHER INFORMATION:
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65 Met Pro Ser Ile Lys Leu Gln Ser Ser Asp Gly Glu Ile Phe Glu Val
66 1           5           10           15
69 Asp Val Glu Ile Ala Lys Gln Ser Val Thr Ile Lys Thr Met Leu Glu
70           20           25           30
73 Asp Leu Gly Met Asp Asp Glu Gly Asp Asp Asp Pro Val Pro Leu Pro

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74          35          40          45
77 Asn Val Asn Ala Ala Ile Leu Lys Lys Val Ile Gln Trp Cys Thr His
78          50          55          60
81 His Lys Asp Asp Pro Pro Pro Pro Glu Asp Asp Glu Asn Lys Glu Lys
82 65          70          75          80
85 Arg Thr Asp Asp Ile Pro Val Trp Asp Gln Glu Phe Leu Lys Val Asp
86          85          90          95
89 Gln Gly Thr Leu Phe Glu Leu Ile Leu Ala Ala Asn Tyr Leu Asp Ile
90          100          105          110
93 Lys Gly Leu Leu Asp Val Thr Cys Lys Thr Val Ala Asn Met Ile Lys
94          115          120          125
97 Gly Lys Thr Pro Glu Glu Ile Arg Lys Thr Phe Asn Ile Lys Asn Asp
98          130          135          140
101 Phe Thr Glu Glu Glu Glu Ala Gln Val Arg Lys Glu Asn Gln Trp Cys
102 145          150          155          160
105 Glu Glu Lys

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109 <210> SEQ ID NO: 3

110 <211> LENGTH: 1917

111 <212> TYPE: DNA

112 <213> ORGANISM: Homo sapiens

114 <220> FEATURE:

115 <221> NAME/KEY: gene

116 <222> LOCATION: (1)..(1917)

117 <223> OTHER INFORMATION: Human Splicing Factor 1

120 <400> SEQUENCE: 3

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121 atggcgaccg gagcgaacgc cacgccgttg gacttcccaa gtaagaagcg gaagaggagc 60
123 cgctggaacc aagacacaat ggaacagaag acagtgattc caggaatgcc tacagttatt 120
125 cccctggac ttactcgaga acaagaaaaga gcttatatag tgcaactgca gatagaagac 180
127 ctgactcgta aactgcgcac aggagacctg ggcattcccc ctaacctga ggacaggtcc 240
129 ccttcccctg agcccatcta caatagcgag gggaagcggc ttaacaccgc agagttccgc 300
131 accgcgaaaa agctggaaga ggagcggcac aacctcatca cagagatggg tgactcaat 360
133 ccggatttca agccacctgc agattacaaa cctccagcaa cacgtgtgag tgataaagtc 420
135 atgattccac aagatgagta ccagaaaatc aactttgtgg ggctgctcat cgggcccaga 480
137 gggaacaccc tgaagaacat agagaaggag tgcaatgcca agattatgat ccgggggaaa 540
139 gggctctgtg aagaagggaa ggttgggcgc aaagatggcc agatgttgcc aggagaagat 600
141 gagccacttc atgccctggt tactgccaat acaatggaga acgtcaaaaa ggcagtggaa 660
143 cagataagaa acatcctgaa gcagggtatc gagactccag aggaccagaa tgatctacgg 720
145 aagatgcagc ttcgggagtt ggctcgctta aatgggaccc ttcgggaaga cgataacagg 780
147 atcttaagac cctggcagag ctacagagacc cgcagcatta ccaacaccac agtgtgtacc 840
149 aagtgtggag gggctggcca cattgcttca gactgtaaat tccaaaggcc tgggtgatcct 900
151 cagtcagctc aggataaagc acggatggat aaagaatatt tgtccctcat ggctgaactg 960
153 ggtgaagcac ctgtcccagc atctgtgggc tccacctctg ggctgcccac cacacccctg 1020
155 gccagcgcac ctgctcctgc tgctcccgcc aacaacccac ctccaccgtc tctcatgtct 1080
157 accaccagaa gccgcccacc ctggatgaat tctggccctt cagagagtcg gccctaccac 1140
159 ggcatgcatg gaggtggtcc tgggtggccc ggaggtggcc cccacagctt cccacaccca 1200
161 ttaccagacc tgacaggtgg gcatggtgga catcccatgc agcacaaccc caatggaccc 1260
163 ccacccctt ggatgcagcc accaccacca ccgatgaacc agggccccc cctcctggg 1320
165 caccatggcc ctctccaat ggatcagtac ctgggaagta cgctgtggg ctctggggtc 1380
167 tatgcctgc atcaaggaaa aggtatgatg ccgccaccac ctatgggcat gatgccgccg 1440

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171 caacaacagc agcagcagcc tccgccccc cctccgccc gcagcagtat ggcttccagt 1560
173 acccccttgc catggcagca aaatacgacg actaccacca cgagcgctgg cacaggggcc 1620
175 atcccgcgat ggcaacagca gcaggcggt gccgcagctt ctccaggagc ccctcagatg 1680
177 caaggcaacc ccaactatggt gcccctgccc cccgggggtcc agccgcctct gccgcctggg 1740
179 gcccctcccc ctcgcgcgccc tccaccgctt ggttcgcgcg gcatgatgat cccctccccg 1800
181 ggcggcgatg gcccagagcca tgagagttag gactttccgc gccatttgtt gacccttcca 1860
183 ggcagacagc ctcagcaacg cccctggtgg acaggatggt tcggcaaacg agcctga 1917

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186 <210> SEQ ID NO: 4

187 <211> LENGTH: 638

188 <212> TYPE: PRT

189 <213> ORGANISM: Homo sapiens

191 <220> FEATURE:

W--> 192 <221> NAME/KEY: Human Splicing Factor 1

193 <222> LOCATION: (1)..(638)

194 <223> OTHER INFORMATION:

197 <400> SEQUENCE: 4

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200 1 5 10 15
203 Arg Lys Arg Ser Arg Trp Asn Gln Asp Thr Met Glu Gln Lys Thr Val
204 20 25 30
207 Ile Pro Gly Met Pro Thr Val Ile Pro Pro Gly Leu Thr Arg Glu Gln
208 35 40 45
211 Glu Arg Ala Tyr Ile Val Gln Leu Gln Ile Glu Asp Leu Thr Arg Lys
212 50 55 60
215 Leu Arg Thr Gly Asp Leu Gly Ile Pro Pro Asn Pro Glu Asp Arg Ser
216 65 70 75 80
219 Pro Ser Pro Glu Pro Ile Tyr Asn Ser Glu Gly Lys Arg Leu Asn Thr
220 85 90 95
223 Arg Glu Phe Arg Thr Arg Lys Lys Leu Glu Glu Glu Arg His Asn Leu
224 100 105 110
227 Ile Thr Glu Met Val Ala Leu Asn Pro Asp Phe Lys Pro Pro Ala Asp
228 115 120 125
231 Tyr Lys Pro Pro Ala Thr Arg Val Ser Asp Lys Val Met Ile Pro Gln
232 130 135 140
235 Asp Glu Tyr Pro Glu Ile Asn Phe Val Gly Leu Leu Ile Gly Pro Arg
236 145 150 155 160
239 Gly Asn Thr Leu Lys Asn Ile Glu Lys Glu Cys Asn Ala Lys Ile Met
240 165 170 175
243 Ile Arg Gly Lys Gly Ser Val Lys Glu Gly Lys Val Gly Arg Lys Asp
244 180 185 190
247 Gly Gln Met Leu Pro Gly Glu Asp Glu Pro Leu His Ala Leu Val Thr
248 195 200 205
251 Ala Asn Thr Met Glu Asn Val Lys Lys Ala Val Glu Gln Ile Arg Asn
252 210 215 220
255 Ile Leu Lys Gln Gly Ile Glu Thr Pro Glu Asp Gln Asn Asp Leu Arg
256 225 230 235 240
259 Lys Met Gln Leu Arg Glu Leu Ala Arg Leu Asn Gly Thr Leu Arg Glu
260 245 250 255

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Input Set : A:\PTO.DC.txt

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263 Asp Asp Asn Arg Ile Leu Arg Pro Trp Gln Ser Ser Glu Thr Arg Ser
264                260                265                270
267 Ile Thr Asn Thr Thr Val Cys Thr Lys Cys Gly Gly Ala Gly His Ile
268                275                280                285
271 Ala Ser Asp Cys Lys Phe Gln Arg Pro Gly Asp Pro Gln Ser Ala Gln
272                290                295                300
275 Asp Lys Ala Arg Met Asp Lys Glu Tyr Leu Ser Leu Met Ala Glu Leu
276 305                310                315                320
279 Gly Glu Ala Pro Val Pro Ala Ser Val Gly Ser Thr Ser Gly Pro Ala
280                325                330                335
283 Thr Thr Pro Leu Ala Ser Ala Pro Arg Pro Ala Ala Pro Ala Asn Asn
284                340                345                350
287 Pro Pro Pro Pro Ser Leu Met Ser Thr Thr Gln Ser Arg Pro Pro Trp
288                355                360                365
291 Met Asn Ser Gly Pro Ser Glu Ser Arg Pro Tyr His Gly Met His Gly
292                370                375                380
295 Gly Gly Pro Gly Gly Pro Gly Gly Gly Pro His Ser Phe Pro His Pro
296 385                390                395                400
299 Leu Pro Ser Leu Thr Gly Gly His Gly Gly His Pro Met Gln His Asn
300                405                410                415
303 Pro Asn Gly Pro Pro Pro Pro Trp Met Gln Pro Pro Pro Pro Pro Met
304                420                425                430
307 Asn Gln Gly Pro His Pro Pro Gly His His Gly Pro Pro Pro Met Asp
308                435                440                445
311 Gln Tyr Leu Gly Ser Thr Pro Val Gly Ser Gly Val Tyr Arg Leu His
312                450                455                460
315 Gln Gly Lys Gly Met Met Pro Pro Pro Pro Met Gly Met Met Pro Pro
316 465                470                475                480
319 Pro Pro Pro Pro Pro Ser Gly Gln Pro Pro Pro Pro Pro Ser Gly Pro
320                485                490                495
323 Leu Pro Pro Trp Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro
324                500                505                510
327 Pro Ser Ser Ser Met Ala Ser Ser Thr Pro Leu Pro Trp Gln Gln Asn
328                515                520                525
331 Thr Thr Thr Thr Thr Thr Ser Ala Gly Thr Gly Ser Ile Pro Pro Trp
332                530                535                540
335 Gln Gln Gln Gln Ala Ala Ala Ala Ala Ser Pro Gly Ala Pro Gln Met
336 545                550                555                560
339 Gln Gly Asn Pro Thr Met Val Pro Leu Pro Pro Gly Val Gln Pro Pro
340                565                570                575
343 Leu Pro Pro Gly Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly Ser
344                580                585                590
347 Ala Gly Met Met Ile Pro Pro Arg Gly Gly Asp Gly Pro Ser His Glu
348                595                600                605
351 Ser Glu Asp Phe Pro Arg Pro Leu Val Thr Leu Pro Gly Arg Gln Pro
352                610                615                620
355 Gln Gln Arg Pro Trp Trp Thr Gly Trp Phe Gly Lys Ala Ala
356 625                630                635
359 <210> SEQ ID NO: 5

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/038,010

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TIME: 13:16:30

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Output Set: N:\CRF4\08062002\J038010.raw

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360 <211> LENGTH: 1173
361 <212> TYPE: DNA
362 <213> ORGANISM: mouse p53
364 <220> FEATURE:
365 <221> NAME/KEY: gene
366 <222> LOCATION: (1)..(1173)
367 <223> OTHER INFORMATION: mouse p53 : Tumour suppressor protein
370 <400> SEQUENCE: 5
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373 acatttttcag gcttatggaa actacttcct ccagaagata tcctgccatc acctcactgc      120
375 atggacgatac tgttgctgcc ccaggatgtt gaggagtttt ttgaaggccc aagtgaagcc      180
377 ctccgagtgat caggagctcc tgcagcacag gaccctgtca ccgagacccc tgggccagcg      240
379 gcccctgccc cagccactcc atggcccctg tcatcttttg tcccttctca aaaaacttac      300
381 cagggcaact atggcttcca cctgggcttc ctgcagtcctg ggacagccaa gtctgttatg      360
383 tgcacgtact ctctccctcc caataagcta ttctgccagc tggcgaagac gtgccctgtg      420
385 cagttgtggg tcagcgcac acctccagct gggagccgtg tccgcgccat ggccatctac      480
387 aagaagtcac agcacatgac ggaggtcggtg agacgctgcc cccaccatga gcgctgctcc      540
389 gatggtgatg gcctggctcc tcccagcat cttatccggg tgggaaggaaa tttgtatccc      600
391 gagtatctgg aagacaggca gacttttcgc cacagcgtgg tggtaacctt tgagccaccc      660
393 gaggccggct ctgagtatac caccatccac tacaagtaca tgtgtaatag ctctgcatg      720
395 gggggcatga accgccgacc tatccttacc atcatcacac tgggaagactc cagtgggaac      780
397 cttctgggac gggacagctt tgaggttcgt gtttgtgcct gccctgggag agaccgccgt      840
399 acagaagaag aaaatttccg caaaaaggaa gtcccttgcc ctgaactgcc cccagggagc      900
401 gcaaagagag cgctgcccac ctgcacaagc gcctctcccc cgcaaaagaa aaaaccactt      960
403 gatggagagt atttcaccct caagatccgc gggcgtaaac gcttcgagat gttccgggag     1020
405 ctgaatgagg ccttagagtt aaaggatgcc catgctacag aggagtctgg agacagcagg     1080
407 gctcactcca gctacctgaa gaccaagaag ggccagtcta cttcccgcga taaaaaaaaca     1140
409 atggtcaaga aagtggggcc tgactcagac tga                                     1173
412 <210> SEQ ID NO: 6
413 <211> LENGTH: 390
414 <212> TYPE: PRT
415 <213> ORGANISM: mouse p53
417 <220> FEATURE:
W--> 418 <221> NAME/KEY: p53
419 <222> LOCATION: (1)..(390)
420 <223> OTHER INFORMATION:
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429 Leu Ser Gln Glu Thr Phe Ser Gly Leu Trp Lys Leu Leu Pro Pro Glu
430          20          25          30
433 Asp Ile Leu Pro Ser Pro His Cys Met Asp Asp Leu Leu Leu Pro Gln
434          35          40          45
437 Asp Val Glu Glu Phe Phe Glu Gly Pro Ser Glu Ala Leu Arg Val Ser
438          50          55          60
441 Gly Ala Pro Ala Ala Gln Asp Pro Val Thr Glu Thr Pro Gly Pro Ala
442 65          70          75          80
445 Ala Pro Ala Pro Ala Thr Pro Trp Pro Leu Ser Ser Phe Val Pro Ser
446          85          90          95

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/038,010

DATE: 08/06/2002

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L:58 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:192 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:418 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:604 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:794 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
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L:2023 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44
L:2129 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:46
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